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Editorial

Editorial: Special Issue on Algorithms for Sequence Analysis and Storage

Veli Mäkinen

Helsinki Institute for Information Technology HIIT, Department of Computer Science, P. O. Box 68 (Gustaf Hållströmin katu 2b), University of Helsinki, Helsinki 00014, Finland;

E-Mail: vmakinen@cs.helsinki.fi

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Abstract: This special issue of *Algorithms* is dedicated to approaches to biological sequence analysis that have algorithmic novelty and potential for fundamental impact in methods used for genome research.

Keywords: high-throughput sequencing; compressed index structures; pattern discovery; population simulation; dynamic programming

1. Introduction

Analysis of high-throughput sequencing data has become a crucial component in genome research. For example, methods based on latest developments in compressed data structures, namely index structures exploiting Burrows-Wheeler transform, are widely deployed in the discovery of disease causing mutations. The success of such approaches is due to being able to solve the dilemma of the indexing requiring more space than the data itself, where the data itself is enormous. With our already increased knowledge about the genomic structure of the whole human population, and with the development of sequencing techniques and their applications in studying RNAs, metapopulations, and epigenetics, the field seeks new innovative and universal algorithmic approaches that assess current and future needs in the analysis and storage of biological sequences.

2. Special Issue

In response to the call for papers, ten articles were submitted to the special issue. Each article was reviewed by at least two anonymous reviewers, and after one to two review rounds, six articles

were selected for the special issue. The range of topics of accepted papers widely covers the analysis and storage theme: the authors contributed in compression of sequencing data [1], compressed index structures [2], pattern/motif discovery [3,4], population simulation [5], and with a novel framework for dynamic programming [6].

Acknowledgments

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Conflicts of Interest

The authors declare no conflict of interest.

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